

SEQUENCE LISTING

<110> OSTERMEIER, MARC A.
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10/588,114
<141> 2006-07-27

<150> PCT/US05/002633
<151> 2005-01-28

<150> 60/628,997
<151> 2004-11-18

<150> 60/607,684
<151> 2004-09-07

<150> 60/557,152
<151> 2004-03-26

<150> 60/539,774
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<170> PatentIn Ver. 3.3

<210> 1
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peptide linker

<400> 1
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<210> 2
<211> 37
<212> PRT
<213> Homo sapiens

<400> 2
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
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Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
20 25 30

Met Gly Leu Leu Thr
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<210> 3
<211> 14
<212> PRT
<213> Rous sarcoma virus

<400> 3
Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
1 5 10

<210> 4
<211> 25
<212> PRT
<213> Unknown Organism

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<223> Description of Unknown Organism: GRK6 peptide
sequence

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1 5 10 15
Asp Ser Glu Glu Glu Leu Pro Thr Arg
20 25

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<211> 7
<212> PRT
<213> Monkey virus SV40

<400> 5
Pro Lys Lys Lys Lys Lys Val
1 5

<210> 6
<211> 6
<212> PRT
<213> Homo sapiens

<400> 6
Ala Arg Arg Arg Arg Pro
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<210> 7
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: NF kappa-B p50
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Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
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<212> PRT
<213> Unknown Organism

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Glu Glu Lys Arg Lys Arg Thr Tyr Glu
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<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Nucleoplasmin
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Lys Lys Lys Leu Asp
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<212> PRT
<213> Homo sapiens

<400> 10
Lys Phe Glu Arg Gln
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<210> 11
<211> 36
<212> PRT
<213> Homo sapiens

<400> 11
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Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
20 25 30

Tyr Gln Thr Ile
35

<210> 12
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<213> Homo sapiens

<400> 12
Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
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<210> 13
<211> 27
<212> PRT
<213> *Saccharomyces cerevisiae*

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Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
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<210> 14
<211> 25
<212> PRT
<213> *Saccharomyces cerevisiae*

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Thr Leu Cys Ser Ser Arg Tyr Leu Leu
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<213> *Saccharomyces cerevisiae*

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Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
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<210> 16

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<212> PRT

<213> *Saccharomyces cerevisiae*

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Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
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Gln Gln Gln Gln Arg Gly Lys Lys
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<223> Description of Unknown Organism: Endoplasmic
reticulum localizing sequence

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<210> 18

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<213> Human adenovirus type 19

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Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
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<210> 19

<211> 20

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: Interleukin-2
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<210> 20

<211> 29

<212> PRT

<213> Homo sapiens

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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
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<210> 21

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<212> PRT

<213> Homo sapiens

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1 5 10 15Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
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<210> 22

<211> 18

<212> PRT

<213> Influenza A virus

<400> 22

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
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Gln Ile

<210> 23

<211> 24

<212> PRT

<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Interleukin-4
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Cys Ala Gly Asn Phe Val His Gly
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<210> 24
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<220>
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primer

<400> 24
tgccggatcc ggccgtggcc acccagaaac gctggtg 37

<210> 25
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<212> DNA
<213> Artificial Sequence

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<210> 26
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<223> Description of Artificial Sequence: Synthetic
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<210> 29
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<223> Description of Artificial Sequence: Synthetic
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| <210> 34 | | |
| <211> 36 | | |
| <212> DNA | | |
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<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 34
 atccggacta gtaggccttt acttggtgat acgagt 36

<210> 35
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 <212> DNA
 <213> Escherichia coli

<400> 35
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 aaaggctata acggctcgc tgaagtcgg aagaaattcg agaaagatac cggaaattaaa 180
 gtcaccgttgc agcatccggaa taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
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 ggtgaaatca tgccgaacat cccgcagatg tccgcttctt ggtatgccgt gcgtactcgc 1920
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 cgtatcacca agtaa 1995

<210> 36
 <211> 664
 <212> PRT
 <213> Escherichia coli

<400> 36
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Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60

His Pro Asp Lys Leu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
 340 345 350

Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
 355 360 365

Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
 370 375 380

Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
 385 390 395 400

Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
 405 410 415

Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
 420 425 430

Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
 435 440 445

Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
 450 455 460

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 465 470 475 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
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Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
 515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
 545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
 565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
 580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
 595 600 605

Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met
 610 615 620

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Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala
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Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys
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Asp Ala Gln Thr Arg Ile Thr Lys
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gtcaccgttgc agcatccgga taaactggaa gagaaaattcc cacaggtgc ggcaactggc 240
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<212> PRT
<213> Escherichia coli
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 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
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 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430
 Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
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 515 520 525
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560
 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
 565 570 575
 Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
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Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
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Gln Thr Arg Ile Thr Lys
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<211> 660

<212> PRT

<213> Escherichia coli

<400> 40

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| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr |
| 1 | | | | | | | | | | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | | | | | | | | 30 |
| | | | | | | | | 20 | | 25 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | | | | | | | | 45 |
| | | | | | | | | 35 | | 40 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | | | | | | | | | | | | | | | 60 |
| | | | | | | | | 50 | | 55 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| | | | | | | | | | | | | | | | 80 |
| | | | | | | | | 65 | | 70 | | 75 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | | | | | | | | | | | | 95 |
| | | | | | | | | 85 | | 90 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | | | | | | | | 110 |
| | | | | | | | | 100 | | 105 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | Ala | Val | Arg | Tyr | Asn | Gly | Lys |
| | | | | | | | | | | | | | | | 125 |
| | | | | | | | | 115 | | 120 | | 125 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu | Ala | Leu | Ser | Leu | Ile | Tyr | Asn |
| | | | | | | | | | | | | | | | 140 |
| | | | | | | | | 130 | | 135 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | Thr | Trp | Glu | Glu | Ile | Pro | Ala |
| | | | | | | | | | | | | | | | 160 |
| | | | | | | | | 145 | | 150 | | 155 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Lys | Glu | Leu | Lys | Ala | Lys | Gly | Lys | Ser | Ala | Leu | Met | Phe | Asn |
| | | | | | | | | | | | | | | | 175 |
| | | | | | | | | 165 | | 170 | | | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Glu | Pro | Tyr | Phe | Thr | Trp | Pro | Leu | Ile | Ala | Ala | Asp | Gly | Gly |
| | | | | | | | | | | | | | | | 190 |
| | | | | | | | | 180 | | 185 | | 190 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Phe | Lys | Tyr | Glu | Asn | Gly | Lys | Tyr | Asp | Ile | Lys | Asp | Val | Gly |
| | | | | | | | | | | | | | | | 205 |
| | | | | | | | | 195 | | 200 | | 205 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Asn | Ala | Gly | Ala | Lys | Ala | Gly | Leu | Thr | Phe | Leu | Val | Asp | Leu |
| | | | | | | | | | | | | | | | 220 |
| | | | | | | | | 210 | | 215 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Asn | Lys | His | Met | Asn | Ala | Asp | Thr | Asp | Tyr | Ser | Ile | Ala | Glu |
| | | | | | | | | | | | | | | | 240 |
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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Phe | Asn | Lys | Gly | Glu | Thr | Ala | Met | Thr | Ile | Asn | Gly | Pro | Trp |
| | | | | | | | | | | | | | | | 255 |
| | | | | | | | | 245 | | 250 | | 255 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Trp | Ser | Asn | Ile | Asp | Thr | Ser | Lys | Val | Asn | Tyr | Gly | Val | Thr | Val |
| | | | | | | | | | | | | | | | 270 |
| | | | | | | | | 260 | | 265 | | 270 | | | |

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 340 345 350

Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 355 360 365

Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 370 375 380

Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 385 390 395 400

Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 405 410 415

Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
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Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
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Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr
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Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly
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Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg
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Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys
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Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg
 515 520 525

Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr
 530 535 540

Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala
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Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr
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 580 585 590
 His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ala
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 Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala
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aagtaa

1986

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 35 40 45
 Val Gly Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
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 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
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 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
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 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
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 340 345 350
 Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu
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 Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr
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 Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala
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 Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu
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 465 470 475 480
 Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe
 485 490 495
 Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu
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 Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly
 515 520 525
 Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val
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 545 550 555 560

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 580 585 590

Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala
 595 600 605

Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile
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Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn
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 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
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 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
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 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asn Glu
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 Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala
 225 230 235 240

Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser
 245 250 255
 Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro
 260 265 270
 Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser
 275 280 285
 Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro
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 Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln
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 Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser
 325 330 335
 Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr Leu Val Lys Val
 340 345 350
 Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu
 355 360 365
 Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg
 370 375 380
 Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu
 385 390 395 400
 Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr
 405 410 415
 Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu
 420 425 430
 Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met
 435 440 445
 Ser Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr Ile Gly Gly Pro
 450 455 460
 Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg
 465 470 475 480
 Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Val Asp Leu Ile Lys
 485 490 495
 Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala
 500 505 510
 Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp
 515 520 525
 Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro
 530 535 540

Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala
 545 550 555 560

Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu
 565 570 575

Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp
 580 585 590

Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala
 595 600 605

Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu
 610 615 620

Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg
 625 630 635 640

Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala
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<210> 45

<211> 1989

<212> DNA

<213> Escherichia coli

<400> 45

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 <211> 662
 <212> PRT
 <213> Escherichia coli

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 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
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 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala
 225 230 235 240
 Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr
 245 250 255
 Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val
 260 265 270
 Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala
 275 280 285
 Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala
 290 295 300
 Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr
 305 310 315 320
 Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile
 325 330 335
 Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr Leu
 340 345 350
 Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr
 355 360 365
 Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro
 370 375 380
 Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly
 385 390 395 400
 Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg
 405 410 415
 Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu
 420 425 430
 Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala
 435 440 445
 Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile
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 Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His
 465 470 475 480
 Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala His Met
 485 490 495
 Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly
 500 505 510
 Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp
 515 520 525

Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly
 530 535 540
 Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala
 545 550 555 560
 Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu
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 Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly
 580 585 590
 Ala Val Ala Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg
 595 600 605
 Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
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 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
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 Gln Thr Arg Ile Thr Lys
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 <212> DNA
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<210> 48

<211> 662

<212> PRT

<213> *Escherichia coli*

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 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
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Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
 340 345 350

Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
 355 360 365

Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
 370 375 380

Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
 385 390 395 400

Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
 405 410 415

Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
 420 425 430

Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
 435 440 445

Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
 450 455 460

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 465 470 475 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
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Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
 515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
 545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
 565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
 580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
 595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
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Gln Thr Arg Ile Thr Lys
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<210> 49

<211> 2007

<212> DNA

<213> Escherichia coli

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<210> 50

<211> 668

<212> PRT

<213> Escherichia coli

<400> 50

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 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
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Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Asn Glu Ala Ile Pro Asn
 340 345 350

Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg
 355 360 365

Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu
 370 375 380

Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser
 385 390 395 400

Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu
 405 410 415

Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro
 420 425 430

Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp
 435 440 445

Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His
 450 455 460

Trp Asp Lys Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu
 465 470 475 480

Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser
 485 490 495

Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met
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Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp
 515 520 525

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Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met
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Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr
 565 570 575

Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr
 580 585 590

Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp
 595 600 605

Glu Pro Glu Leu Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys
 610 615 620

Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 625 630 635 640

Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 645 650 655

Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
 660 665

<210> 51
 <211> 1989
 <212> DNA
 <213> Escherichia coli

<400> 51
 atgaaaataa aaacagggtc acgcattcctc gcattatccg cattaacgac gatgatgtt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acgggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaaattaaa 180
 gtcaccgttg agcatccgaa taaaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aatatcccccc ggacaaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttacccga tcgctgttga agcgttatcg 420
 ctgattata acaaagatct gctgccgaac ccggccaaaaa cctgggaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcaccc ggcgcgtat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcggtggat aacgctggcg cgaaagcggg tctgaccctc 660
 ctgggttggacc tgattaaaaa caaacacatg aatgcagacca ccgattactc catcgccagaa 720
 gctgccttta ataaaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaac 780
 atcgacacca gcaaagtggaa ttatgggtgtc acgggtactgc cgaccccaa gggtcaacca 840
 tccaaaccgt tcgttggcgt gctgagcgcgaa ggtatggatcc cccgcagtcgaa acacaaagag 900
 ctggcgaaag agttccctcga aaactatctg ctgactgtatc aaggcttgcgaa agcgggttaat 960
 aaagacaaac cgctgggtgc cgtagcgcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
 ccacgtaatg aagccatacc aaacgacgag cgtgacacca cgtgcctgc agcaatggca 1080

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acaacgttgc gcaaactatt aactggcgaa ctacttactc tagctcccg gcaacaatta 1140
atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc cttccggct 1200
ggctgggta ttgctgataa atctggagcc ggtgagcgtg ggtctcgccg tattattgca 1260
gcactgggac cagatggtaa gccctccgt atcgtagtta tctacacgac ggggagtcag 1320
gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
tgggacaaga gccacccaga aacgctgggt aaagtaaaag atgctgaaga tcagttgggt 1440
gcacgagtgg gttacatgca actggatctc aacagcggta agatccttga gagttttcgc 1500
cccgaaagaac gtttccaat gatgagcaact tttaaagttc tgctatgtgg cgcggatatta 1560
tcccggtttg acgccccggca agagcaactt ggtcgccgca tacacttac tacaaatgac 1620
ttgggtttagt actcaccagt cacagaaaaag catcttacgg atggcatgac agtaagagaa 1680
ttatgcgtg ctgcattaaac catgagtgtat aacactgcgg ccaacttact tctgacaacg 1740
atcgaggagac cgaaggagct aaccgcgtttt ttgcacaaca tggggatca tgtaactcgc 1800
cttgatcggtt gggAACCGGA actgaatgaa gcccacatgg aaaacgccc aaaaagggtgaa 1860
atcatgccga acatcccgca gatgtccgct ttctggatg ccgtgcgtac tgcgggtgatc 1920
aacggcccca gcggtcgatc gactgtcgat gaagccctga aagacgccc gactcgatc 1980
accaaatggaa

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<210> 52
<211> 662
<212> PRT
<213> Escherichia coli
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<400> 52
Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
20 25 30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
65 70 . 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Ile Ile Tyr Asn
130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
 340 345 350
 Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
 355 360 365
 Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
 370 375 380
 Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
 385 390 395 400
 Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
 405 410 415
 Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
 420 425 430
 Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
 435 440 445
 Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
 450 455 460
 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 465 470 475 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 485 490 495
 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
 500 505 510
 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
 515 520 525
 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 530 535 540
 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
 545 550 555 560
 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
 565 570 575
 Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
 580 585 590
 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
 595 600 605
 Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620
 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640
 Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655
 Gln Thr Arg Ile Thr Lys
 660

<210> 53
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

 <400> 53
 atgaaaataa aaacaggtgc acgcacccctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcttg 120
 tttggctata acggctcgc tgaagtcgg aagaaattcg agaaagatac cgaaattaaa 180
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aaatcaccgg ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccgg a tcgctgttta tgcgttatcg 420
 ctgattata acaaagatct gctgccgaac ccgcggaaaa cctggaaaga gatcccgccg 480
 ctggataaaag aactgaaagc gaaaggtaaag agcgcgctga tgttcaacct gcaagaacccg 540
 tacttcaccc ggcgcgtat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca taaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccctc 660

| | | | | | | |
|-------------|-------------|-------------|-------------|--------------|-------------|------|
| ctgggttacc | tgattaaaaa | caaacacatg | aatgcagaca | ccgattactc | catgcagaa | 720 |
| gctgcctta | ataaaaggcga | aacagcgatg | accatcaacg | gccccgtggc | atggtccaac | 780 |
| atcgacacca | gcaaagtgaa | ttatgggtga | acggtaactgc | cgaccccaa | gggtcaacca | 840 |
| tccaaaccgt | tcgttggcgt | gctgagcga | ggtattaaacg | ccgccaagtcc | gaacaaagag | 900 |
| ctggcggaaag | agttcctcga | aaactatctg | ctgactgatg | aaggcttgg | agcggtaat | 960 |
| aaagacaaaac | cgctgggtgc | cgtagcgctg | aagtcttacg | aggaagagtt | ggcggaaagat | 1020 |
| ccacgtgcca | tacccaaacga | cgagcgtgac | accacgatgc | ctgcagcaat | ggcaacaacg | 1080 |
| ttgcgcaaac | tattaactgg | cgaactactt | actcttagctt | cccgccaaca | attaatagac | 1140 |
| tggatggagg | cggataaaagt | tgcaggacca | cttctgcgc | cggcccttcc | ggctggctgg | 1200 |
| tttattgtctg | ataaaatctgg | agccggtgag | cgtgggtctc | gcccgttatcat | tcagcactg | 1260 |
| ggggccagatg | gtaagccctc | ccgtatcgta | gttatctaca | cgacggggag | tcaggcaact | 1320 |
| atggatgaac | gaaatagaca | gatcgctgag | ataggtgcct | cactgattaa | gcattgggac | 1380 |
| aagagccacc | cagaacacgt | ggtggaaagta | aaagatgctg | aagatcagg | gggtgcacga | 1440 |
| gtgggttaca | tcgaaactgg | tctcaacacgc | ggtaagatcc | ttgagagttt | tcggccggaa | 1500 |
| gaaacgtttc | caatgatgag | cactttaaa | gttctgttat | gtggcccggt | attatcccg | 1560 |
| gttgcacccg | ggcaagagca | actcggtcgc | cgcatacact | attctcagaa | tgacttggg | 1620 |
| gagtaactcac | cagtccacaga | aaagcatctt | acggatggca | tgacagtaag | agaattatgc | 1680 |
| agtgcgtcca | taaccatgag | tgataaacact | gcccccaact | tacttctgac | aacgatcgcga | 1740 |
| ggaccgaaagg | agctaaccgc | ttttttgcac | aacatggggg | atcatgttaac | tcgccttgc | 1800 |
| cgttgggaac | cggaaactgaa | tgaagccgc | gccaccatgg | aaaaccccc | gaaagggtgaa | 1860 |
| atcatgccga | acatcccgca | gatgtccgt | ttctggat | ccgtgcgtac | tcgggtgatc | 1920 |
| aacccgcaca | cgccgtcgta | gactgtcgat | gaagccctga | aagacgcgc | gactcgtatc | 1980 |
| accaagtaa | | | | | | 1989 |

<210> 54

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 54

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
20 25 30

Leu Val Ile Trp Ile Asn Gly Leu Phe Gly Tyr Asn Gly Leu Ala Glu
35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
65 70 75 80

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Tyr Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430

Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 500 505 510
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560
 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu
 565 570 575
 Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605
 Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620
 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640
 Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655
 Gln Thr Arg Ile Thr Lys
 660

<210> 55
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 55
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30

Leu Val Ile Trp Ile Asn Gly Leu Gln Gly Tyr Asn Gly Leu Ala Glu
 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Gln Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350

Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365

Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380

Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400

Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415

Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430

Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445

Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 500 505 510

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540

Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu
 565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655

Gln Thr Arg Ile Thr Lys
 660

<210> 56
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 56
 atgaaaataa aaacaggtgc acgcacccgc gcattatccg cattaacgcac gatgatgtt 60
 tccgcctcggt ctctcgccaa aatcgaaagaa ggtaaactgg taatctggat taacggcaag 120
 gagggtata acggtctcggt tgaagtcgggt aagaaattcg agaaagatac cgaaattaaa 180
 gtcaccgttg agcatccggaa taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aaatcaccggc ggacaaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccggc tcgctgttgc ggcgttatcg 420
 ctgatttata acaaagatct gctggcgaac ccggccaaaaa cctggaaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaaag agcgcgctgat tggtcaaccc gcaagaaccg 540
 tacttcaccc ttgcgcgtat tgctgctgac gggggttatg cgttcaagtg taaaacggc 600
 aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcgcc tctgaccc 660
 ctggttgacc tgattaaaaaa caaacacatg aatgcagaca ccgattactc catcgccagaa 720
 gctgcctta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaaac 780
 atcgacacca gcaaagtggaa ttatgggtgta acgggtactgc cgaccccaa gggtcaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggttattaaacg ccgcgcgtcc gaacaaagag 900
 ctggcggaaag agttccctcgaa aactatctg ctgactgtatc aaggctggaa agcggttatc 960
 aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagatggcggaaagat 1020
 ccacgtgcca taccaaacgca cgagcggtgac accacgatgc ctgcgcgaaat ggcaacaaacg 1080
 ttgcgcggaaac tattaaactgg cgaactactt actcttagttt cccggcaaca attaatagac 1140
 tggatggagg cggataaagt tgccaggacca ttctgcgtt cggcccttcc ggctggctgg 1200
 ttatgtctg ataaatctgg agccgggtgag cgtgggtctc gcggtatcat tgccgcactg 1260
 gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
 atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
 aagagccacc cagaaacgct ggtgaaagta aaagatgtcg aagatcgtt ggggcacgaa 1440
 gtgggttaca tcgaaactgta tctcaacacg ggtaaagatcc ttgagagttt tcggcccgaa 1500
 gaacgttttc caatgtatgag cactttaaa gttctgcata gtggcgccgtt attatccgt 1560
 gttgacgccc ggcaagagca actcggtcgc cgccataactt attctcagaa tgacttgggt 1620
 gagtactcac cagtcacaga aaagatctt acggatggca tgacagtaag agaattatgc 1680
 agtgcgtgcca taaccatgag tgataacact gcccggcaact tacttctgac aacgatcgaa 1740
 ggaccgaaagg agctaaccgc tttttgcac aacatggggg atcatgtac tcgccttgat 1800
 cggtggaaac cggaaactgaa tgaagccgcc gcccacatgg aaaacgccc gaaagggtgaa 1860
 atcatgcccga acatcccgca gatgtccgct ttctggatg ccgtgcgtac tgccgtgatc 1920
 aacgcccggca gcccggcgtca gactgtcgat gaagccctgaa aagacgccc gactcgtatc 1980
 accaagtaa 1989

<210> 57
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 57
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Lys Glu Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Arg Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430
 Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 500 505 510
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu
 565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655

Gln Thr Arg Ile Thr Lys
 660

<210> 58

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 58

atgaaaataa aaacagggtgc acgcacccctc gcattatccg cattaacgc gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcttg 120
 gagggtctaa acggctctcg tgaagtcggg aagaaattcg agaaagatac cggaatttaaa 180
 gtcacccgttgc agcatccgga taaactggaa gagaatttcc cacaggttgc ggcaactggc 240
 gatggccctg acattatcc ctatgcacac gaccgcggg tgggttacgc tcaatctggc 300
 ctgttggctg aatcacccccc ggacaaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacccg caaagtggatt gcttaccggaa tcgctgttgc tgcgttatcg 420
 ctgatttata acaaagatct gctgccgaac cggccaaaaaa cctggaaaga gatcccggcg 480
 ctggataaaag aactgaaagc gaaaggtaag agcgcgctga tggtaaacct gcaagaacccg 540
 tacttcaccc ggcgcgtat tgctgtgac gggggttatg cgttcaagta tggaaacccg 600
 aagtacgaca ttaaagacgt gggcggttatg aacgcgtggcg cggaaacccg 660
 ctgggtgacc tgattaaaaaa caaacacatg aatgcagaca ccgattactc catcgccagaa 720
 gctgcctta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaa 780
 atcgacacca gcaaaatgttgc ttatgggtgtt acgggtactgc cgaccccaa gggtaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaaacg cccgcagtcgaa 900
 ctggcgaaag agttccctcgaa aactatctg ctgactgtatg aaggtctggaa agcgggttaat 960
 aaagacaaac cgctgggtgc cgtacgcgtg aagtcttacg aggaagatggcggaaagat 1020
 ccacgtgcca taccaaaccga cgagcggtac accacgtatgc ctgcagcaat ggcaacaacg 1080
 ttgcgcacaaac tattaactgg cgaactactt actcttagtt cccggcaaca attaatagac 1140
 tggatggagg cggataaaatgttgc tgcaggacca cttctgcgtt cggcccttcc ggctggctgg 1200
 tttatttgcg ataaatctgg agccgggtgag cgtgggttcc gcggttatcat tgcagcactg 1260
 gggccagatg gtaaggccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
 atggatgaac gaaatagaca gatcgctgag atagggtgcct cactgattaa gcattgggac 1380
 aagagccacc cagaaacgct ggtgaaagta aaagatgcgtg aagatcagtt gggtgcacga 1440
 gtgggttaca tcgaactggaa tctcaacagc ggtaaagatcc ttgagagttt tcgccccgaa 1500
 gaacgttttc caatgtatgag cactttaaa gttctgctat gtggcgccgtt attatcccg 1560

gttgcgcgg ggcaagagca actcggtcg cgcatacact attctcagaa tgacttggtt 1620
 gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
 agtgctgcca taaccatgag tgataaacact gcggccaact tacttctgac aacgatcgga 1740
 ggaccgaagg agctaaccgc tttttgcac aacatggggg atcatgtaac tcgccttgat 1800
 cgttggaaac cggaaactgaa tgaagccgcc gccaccatgg aaaacgccc gaaaggtgaa 1860
 atcatgcccga acatcccgca gatgtccgct ttctggatg ccgtgcgtac tgccgtgatc 1920
 aacgcccga gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
 accaagtaa 1989

<210> 59

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 59

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr |
| 1 | | | | | | | | | | | | | | | 15 |
| 5 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | | | | | | | | 30 |
| 20 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Leu | Glu | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | | | | | | | | 45 |
| 35 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Gly | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu | |
| | | | | | | | | | | | | | | | 50 |
| 55 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| | | | | | | | | | | | | | | | 80 |
| 65 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Tyr | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | | | | | | | | | | | | 95 |
| 85 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | | | | | | | | 110 |
| 100 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | Ala | Val | Arg | Tyr | Asn | Gly | Lys |
| | | | | | | | | | | | | | | | 115 |
| 120 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Arg | Ala | Leu | Ser | Leu | Ile | Tyr | Asn |
| | | | | | | | | | | | | | | | 130 |
| 135 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | Thr | Trp | Glu | Glu | Ile | Pro | Ala |
| | | | | | | | | | | | | | | | 145 |
| 150 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Lys | Glu | Leu | Lys | Ala | Lys | Gly | Lys | Ser | Ala | Leu | Met | Phe | Asn |
| | | | | | | | | | | | | | | | 165 |
| 170 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Glu | Pro | Tyr | Phe | Thr | Trp | Pro | Leu | Ile | Ala | Ala | Asp | Gly | Gly |
| | | | | | | | | | | | | | | | 180 |
| 185 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Phe | Lys | Tyr | Glu | Asn | Gly | Lys | Tyr | Asp | Ile | Lys | Asp | Val | Gly |
| | | | | | | | | | | | | | | | 195 |
| 200 | | | | | | | | | | | | | | | |

205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350

Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365

Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380

Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400

Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415

Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430

Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445

Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 500 505 510

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540

Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu
 565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655

Gln Thr Arg Ile Thr Lys
 660

<210> 60

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 60

atgaaaataa aaacagggtgc acgcacccgc gcattatccg cattaaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggctctcg tgaagtcggta aagaaattcg agaaagatac cgaaattaaa 180
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aaatcaccccc ggacaaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttacccga tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgcacaaaaa cctggaaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tggtaaacct gcaagaaccg 540
 tacttcaccc ggcgcgtat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcggtggat aacgctggcg cgaaagcggg tctgaccc 660
 ctgggttggacc tgattaaaaaa caaacacatg aatgcagaca ccgattactc catcgccagaa 720
 gctgcctta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaaac 780
 atcgacacca gcaaagtggaa ttatgggtgtc acggtaactgc cgacccttcaa gggtaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccggcagtcgaa acacaaagag 900
 ctggcggaaag agttcctcga aaactatctg ctgactgtatg aaggctgttgc agcggtaat 960
 aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaaagat 1020

ccacgctgg tattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt 1080
 gcagcaactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
 caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
 cattggggat cccggcggtgg ccaccagaa acgctggtga aagtaaaaaga tgctgaagat 1260
 cagttgggtg cacgagtggtt tacatcgaa ctggatctca acagcggtaa gatcctttag 1320
 agtttcgccc cccagaacaacg ttttccaatg atgagcactt taaaagttct gctatgtggc 1380
 gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcggccat acactattct 1440
 cagaatgact tggttgagta ctcaccagtc acagaaaaagc atcttacgga tggcatgaca 1500
 gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
 ctgacaacga tcggaggacc gaaggagcta accgctttt tgccacaacat gggggatcat 1620
 gtaactcgcc ttgatcggtt ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
 gacaccacga tgcctgcagc aatggcaaca acgttgcgc aactattaac tggcgaacta 1740
 cttactctag cttccggca acaattaata gactggatgg aggccgataa agttgcagga 1800
 ccacttctgc gtcggccct tccggctggc tccggccacca tggaaaaacgc ccagaaaggt 1860
 gaaatcatgc cgaacatccc gcagatgtcc gcttctgtt atgcgtgcg tactgcgggt 1920
 atcaacgccc ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
 atcaccaagt aa 1992

<210> 61

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 61

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr |
| 1 | | | | | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | 20 | | 25 | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | 35 | | 40 | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | | | | | | | | 50 | | 55 | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| | | | | | | | | 65 | | 70 | | | 75 | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | | | | | 85 | | 90 | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | 100 | | 105 | | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | Ala | Val | Arg | Tyr | Asn | Gly | Lys |
| | | | | | | | | 115 | | 120 | | | 125 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu | Ala | Leu | Ser | Leu | Ile | Tyr | Asn |
| | | | | | | | | 130 | | 135 | | | 140 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | Thr | Trp | Glu | Glu | Ile | Pro | Ala |
| | | | | | | | | 145 | | 150 | | | 155 | | 160 |

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly
 340 345 350
 Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys
 355 360 365
 Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met
 370 375 380
 Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys
 385 390 395 400
 His Trp Gly Ser Gly Gly His Pro Glu Thr Leu Val Lys Val Lys
 405 410 415
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 420 425 430
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 435 440 445
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 450 455 460

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 465 470 475 480
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 485 490 495
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 500 505 510
 Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr Ile Gly Gly Pro Lys
 515 520 525
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 530 535 540
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 545 550 555 560
 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 565 570 575
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 580 585 590
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 595 600 605
 Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro
 610 615 620
 Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
 625 630 635 640
 Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
 645 650 655
 Ala Gln Thr Arg Ile Thr Lys
 660

<210> 62
 <211> 1992
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 62
 atgaaaataa aaacaggtgc acgcacccctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcggt ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggctctcg tgaagtcgg aagaaattcg agaaagatac cgaaattaaa 180
 gtcaccgttgc agcatccgaa taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttacccga tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccggaaaaaa cctggaaaga gatccccggcg 480

ctggataaag aactgaaagc gaaaggtaag agcgcgtga tgttcaacct gcaagaaccc 540
 tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccc 660
 ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
 gctgcctta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaac 780
 atcgacacca gcaaagtgaa ttatggtgta acggtaactgc cgaccctcaa gggtcaacca 840
 tccaaaccgt tcgttggcgt gctgagcgc ggtattaaacg ccgcgcgtcc gaacaaagag 900
 ctggcggaaag agttcctcga aaactatctg ctgactgtg aaggcttgaa agcggtaat 960
 aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
 ccacgctggt ttattgtga taaatcttgg a cccgtggc gtgggtctcg cggtatcatt 1080
 gcagcactgg gcccgcgtgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
 cagggacta tggatggaaac aaatagacag atcgctgaga taggtgcctc actgattaag 1200
 cattggggat cccgtggcgtgg ccaccaggaa acgttggta aagttttttt tgctgaagat 1260
 cagttgggtg caccggatgg ttatcgaa ctggatctca acagcggtaa gatccttgag 1320
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 gcggtattat cccgtggta cccggggcaa gagcaactcg gtcgcgcacatattct 1440
 cagaatgact tgggttgagta ctcaccagtc acagaaaacg atcttacgga tggcatgaca 1500
 gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
 ctgacaacga tcggaggacc gaaggagcta accgcgtttt tgcacaacat gggggatcat 1620
 gtaactcgcc ttgatcggtt ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
 gacaccacga tgcctgcagc aatggcaaca acgttgcgc aactattaac tggcgaacta 1740
 cttactctag cttcccgca acaattaata gactggatgg aggccgataa agttgcagga 1800
 ccacttctgc gctcgccct tccggctggc tccggccacca tggaaaacgc ccagaaaggt 1860
 gaatggatgc cgaacatccc gcagatgtcc gctttcttgtt atgcgtgcg tactgcggc 1920
 atcaacgccc ccagcggtcg tcagactgtc gatgaagccc taaaagacgc gcagactcgt 1980
 atcaccaagt aa 1992

<210> 63

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 63

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr |
| 1 | | | | | | | | 5 | | | | | 10 | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | 20 | | | 25 | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | 35 | | | 40 | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | | | | | | | | 50 | | | 55 | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| | | | | | | | | 65 | | | 70 | | 75 | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | | | | | 85 | | | 90 | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | 100 | | | 105 | | 110 | | |

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly
 340 345 350

Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys
 355 360 365

Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met
 370 375 380

Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys
 385 390 395 400

His Trp Gly Ser Gly Gly His Pro Glu Thr Leu Val Lys Val Lys
 405 410 415

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 420 425 430

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 435 440 445

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 450 455 460

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 465 470 475 480

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 485 490 495

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 500 505 510

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 515 520 525

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 530 535 540

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 545 550 555 560

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 565 570 575

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 580 585 590

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 595 600 605

Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Trp Met Pro
 610 615 620

Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
 625 630 635 640

Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
 645 650 655

Ala Gln Thr Arg Ile Thr Lys
 660

<210> 64

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 64

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 aaaggctata acggctcgc tgaagtcggt aagaaattcg agaaagatac cggaaattaaa 180
 gtcaccgttgc agcatccgga taaactggaa gagaattcc cacaggtgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgcttgc gtggctacgc tcaatctggc 300
 ctgttggctg aaatcaccac ggacaaagcg ttccaggaca agctgtatcc gttacctgg 360
 gattgggtac gttacaacgg caagctgatt gcttacccga tcgctgtga agcgatcc 420
 ctgattata acaaagatct gctgccgaac cggccaaaaa cctggaaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaaag agcgcgtc tgctcaaccc gcaagaaccc 540
 tacttcacct ggccgctgat tgctgtcgc gggggatcg ctggctcaagta tgaaaacggc 600
 aagtacgaca taaagacgt gggcgtggat aacgctggcg cggaaacggg tctgaccc 660
 ctgggtgacc tgataaaaaa caaacacatg aatgcagaca cggattactc catcgccaga 720
 gtcgcctta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaa 780
 atcgacacca gcaaagtggaa ttatgggtgta acggctactgc cgaccccaa gggtcaacca 840
 tccaaaccgt tcggtggcgt gctgagcga ggtatccaa cggccagtc gaacaaagag 900
 ctggcggaaag agttcctcga aaactatctg ctgactgatg aaggctggaa agcggttaat 960
 aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
 ccacgctgg tatttgcgta taaatctggaa gcccgtggc gtgggtctcg cggatccatt 1080
 gcagcaactgg ggccagatgg taagccctcc cgtatcgat ttatcttacac gacggggagt 1140
 caggcaacta tggatgaacg aaatagacag atcgctgaga tagtgcctc actgattaag 1200
 cattggggat ccggcgggtgg ccacccagaa acgctggta aagtaaaaga tgctgaagat 1260
 cagttgggtg cacgagtggtt acatcgaa ctggatctca acagcggtaa gatccttgc 1320
 agtttcgccc cccaagaacg ttttccatg atgagcaccc tttaaagttct gctatgtggc 1380
 gcggatttat cccgtgttgc cggccggca gagcaactcg gtcggccat acactattct 1440
 cagaatgact tgggtgatg ctcaccagtc acagaaaagc atcttacggg tggcatgaca 1500
 gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
 ctgacaacga tcggaggacc gaaggagcta accgctttt tgcacaacat gggggatcat 1620
 gtaactcgcc ttgatcgatg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
 gacaccacga tgcctgcagc aatggcaaca acgttgcgc aactattaac tggcgaacta 1740
 cttactcttag cttcccgca acaattaata gactggatgg aggccgataa agttgcagga 1800
 ccacttctgc gtcggccct tccggctggc tccggccacca tggaaaacgc ccagaaagg 1860
 gaatggatgc cgaacatccc gcagatgtcc gcttctggat atgcctgtgc tactgcgggt 1920
 atcaacgccc ccagcggtcg tcagactgtc gatgaagccc tggaaagacgc gcagactcgt 1980
 atcaccaagt aa 1992

<210> 65

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 65

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr |
| 1 | | | | | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | | 40 | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | | | | | | | | | 55 | | | 60 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | 85 | | | | | 90 | | | | 95 | | |
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | 100 | | | | 105 | | | | | 110 | | |
| Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | Trp | Val | Arg | Tyr | Asn | Gly | Lys |
| | | | | 115 | | | | 120 | | | | 125 | | | |
| Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu | Ala | Leu | Ser | Leu | Ile | Tyr | Asn |
| | | | | 130 | | | | 135 | | | | 140 | | | |
| Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | Thr | Trp | Glu | Glu | Ile | Pro | Ala |
| | | | | 145 | | | | 150 | | | 155 | | 160 | | |
| Leu | Asp | Lys | Glu | Leu | Lys | Ala | Lys | Gly | Lys | Ser | Ala | Leu | Met | Phe | Asn |
| | | | | 165 | | | | 170 | | | 175 | | | | |
| Leu | Gln | Glu | Pro | Tyr | Phe | Thr | Trp | Pro | Leu | Ile | Ala | Ala | Asp | Gly | Gly |
| | | | | 180 | | | | 185 | | | | 190 | | | |
| Tyr | Ala | Phe | Lys | Tyr | Glu | Asn | Gly | Lys | Tyr | Asp | Ile | Lys | Asp | Val | Gly |
| | | | | 195 | | | | 200 | | | 205 | | | | |
| Val | Asp | Asn | Ala | Gly | Ala | Lys | Ala | Gly | Leu | Thr | Phe | Leu | Val | Asp | Leu |
| | | | | 210 | | | | 215 | | | 220 | | | | |
| Ile | Lys | Asn | Lys | His | Met | Asn | Ala | Asp | Thr | Asp | Tyr | Ser | Ile | Ala | Glu |
| | | | | 225 | | | | 230 | | | 235 | | 240 | | |
| Ala | Ala | Phe | Asn | Lys | Gly | Glu | Thr | Ala | Met | Thr | Ile | Asn | Gly | Pro | Trp |
| | | | | 245 | | | | 250 | | | 255 | | | | |
| Ala | Trp | Ser | Asn | Ile | Asp | Thr | Ser | Lys | Val | Asn | Tyr | Gly | Val | Thr | Val |
| | | | | 260 | | | | 265 | | | 270 | | | | |
| Leu | Pro | Thr | Phe | Lys | Gly | Gln | Pro | Ser | Lys | Pro | Phe | Val | Gly | Val | Leu |
| | | | | 275 | | | | 280 | | | 285 | | | | |
| Ser | Ala | Gly | Ile | Asn | Ala | Ala | Ser | Pro | Asn | Lys | Glu | Leu | Ala | Lys | Glu |
| | | | | 290 | | | | 295 | | | 300 | | | | |
| Phe | Leu | Glu | Asn | Tyr | Leu | Leu | Thr | Asp | Glu | Gly | Leu | Glu | Ala | Val | Asn |
| | | | | 305 | | | | 310 | | | 315 | | 320 | | |
| Lys | Asp | Lys | Pro | Leu | Gly | Ala | Val | Ala | Leu | Lys | Ser | Tyr | Glu | Glu | Glu |
| | | | | 325 | | | | 330 | | | 335 | | | | |
| Leu | Ala | Lys | Asp | Pro | Arg | Trp | Phe | Ile | Ala | Asp | Lys | Ser | Gly | Ala | Gly |
| | | | | 340 | | | | 345 | | | 350 | | | | |
| Glu | Arg | Gly | Ser | Arg | Gly | Ile | Ile | Ala | Ala | Leu | Gly | Pro | Asp | Gly | Lys |
| | | | | 355 | | | | 360 | | | 365 | | | | |

Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met
 370 375 380

Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys
 385 390 395 400

His Trp Gly Ser Gly Gly His Pro Glu Thr Leu Val Lys Val Lys
 405 410 415

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 420 425 430

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 435 440 445

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 450 455 460

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 465 470 475 480

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 485 490 495

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 500 505 510

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 515 520 525

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 530 535 540

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 545 550 555 560

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 565 570 575

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 580 585 590

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 595 600 605

Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Trp Met Pro
 610 615 620

Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
 625 630 635 640

Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
 645 650 655

Ala Gln Thr Arg Ile Thr Lys
 660

```
<210> 67
<211> 662
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein construct

<400> 67
Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1           5           10           15
```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly His
 180 185 190

Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr
 195 200 205

Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly
 210 215 220

Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr
 225 230 235 240

Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp
 245 250 255

Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys
 260 265 270

Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile
 275 280 285

Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala
 290 295 300

Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg
 305 310 315 320

Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser
 325 330 335
 Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu
 340 345 350
 Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 355 360 365
 Asp Lys Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp
 370 375 380
 Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly
 385 390 395 400
 Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser
 405 410 415
 Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala
 420 425 430
 Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu
 435 440 445
 Val Glu Tyr Ser Pro Val Thr Asp Gly Gly Tyr Ala Phe Lys Tyr Glu
 450 455 460
 Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala
 465 470 475 480
 Lys Ala Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met
 485 490 495
 Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly
 500 505 510
 Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp
 515 520 525
 Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly
 530 535 540
 Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala
 545 550 555 560
 Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu
 565 570 575
 Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly
 580 585 590
 Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg
 595 600 605
 Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

<210> 68
<211> 1995
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 68
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tccgcctcgg ctctcgccaa aatcgaagaa gttaaaactgg taatctggat taacggcgat 120
aaaggctata acggctcgcc tgaagtcggg aagaaattcg agaaagatac cgaaattaaa 180
gtcaccggtt agcatccggaa taaactggaa gagaattcc cacaggtgc ggcaactggc 240
gatggccctg acattatctt ctggcacac gaccgcttg gtggctacgc tcaatctggc 300
ctgttgctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatccgtac gtacaacgg caagctgatt gtttacccga tcgctgttga agcgttatcg 420
ctgattata acaaagatct gctgcccac ccggccaaaaa cctggaaaga gatcccgccg 480
ctggataaaag aactgaaagc gaaaggtaag agcgcgctga ttttcaacct gcaagaaccc 540
tacttccaccc gggcgtatgat tgctgttgc gggcttctgc gtcggccct tccggctggc 600
tggtttattt ctgataaaatc tggagccggg gagcgtgggt ctcgcgttat cattgcagca 660
ctggggccag atggtaagcc ctcccgatc gtatgttatctt acacgacggg gagtcaggca 720
actatggatc aacgaaatag acagatcgat gagatgggtg ctcactgtat taagcattgg 780
ggatccggcg gtggccaccg agaaacgctg gtggaaagtaa aagatgttga agatcgatg 840
ggtgcacgag tgggttacat cgaactggat ctcacacgg gtaagatct tggaggttt 900
cgccccgaag aacgttttc aatgtatggc actttttaaag ttctgtatg tggcgcggta 960
ttatcccgatg ttgacgcggc gcaagagccaa ctcggctgcgc gcatacacta ttctcagaat 1020
gacttgggtt agtactcacc agtcacagaa aagcatctt cggatggcat gacagtaaga 1080
gaattatgcgat gtgtgtccat aaccatgagt gataacactg cggccaaactt acttctgaca 1140
acgatccggag gaccgaagga gctaaccgc ttttgcaca acatggggga tcatgttaact 1200
cgccttgcattt gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc 1260
acgatgcctg cagcaatggc aacaacgtt cgcacaaactt taactggcgta actacttact 1320
ctagctcccc ggcacaaatt aatagactgg atggaggcgat ataaagttgc agacgggggt 1380
tatgcgttca agtatgaaaaa cggcaagtac gacattaaag acgtggcgat ggataacgct 1440
ggcgcgaaag cgggtctgac cttccgtt gacctgatta aaaacaaaca catgaatgca 1500
gacaccgatt actccatcgcc agaagctggc tttataaaag gcaaaacagc gatgaccatc 1560
aacggcccgat gggcatggcc caacatcgac accagcaaa tgaattatgg tgtaacggta 1620
ctggccaccc tcaagggtca accatccaaa cccgttgcgtt gcgtgttgc ggcgggtt 1680
aacggcccca gttccgaacaa agagctggcg aaagagttcc tcgaaaacta tctgttact 1740
gatgaagggtc tggaaagggtt taataaaagac aaaccgctgg gtggcgtagc gctgaagtt 1800
tacgagaaag agttggcgaa agatccacgt attggccgcata ccatggaaaa cgcccgagaaa 1860
ggtaaatca tgccgaacat cccgcagatg tccgctttctt ggtatggcgat ggcgtactg 1920
gtgtcaacgc cccgcagcgat tgcgttact gtcgtatgaa ggcctgaaaga cgccgcagact 1980
cgtatcacca agtaa 1995

<210> 69
 <211> 664
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic...
 protein construct

<400> 69
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Leu
 180 185 190
 Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly
 195 200 205
 Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp
 210 215 220
 Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala
 225 230 235 240
 Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu
 245 250 255

Ile Lys His Trp Gly Ser Gly Gly His Pro Glu Thr Leu Val Lys
 260 265 270
 Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu
 275 280 285
 Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu
 290 295 300
 Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val
 305 310 315 320
 Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His
 325 330 335
 Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His
 340 345 350
 Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr
 355 360 365
 Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly
 370 375 380
 Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr
 385 390 395 400
 Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp
 405 410 415
 Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys
 420 425 430
 Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile
 435 440 445
 Asp Trp Met Glu Ala Asp Lys Val Ala Asp Gly Gly Tyr Ala Phe Lys
 450 455 460
 Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala
 465 470 475 480
 Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys
 485 490 495
 His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn
 500 505 510
 Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn
 515 520 525
 Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe
 530 535 540
 Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile
 545 550 555 560

Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn
 565 570 575

Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro
 580 585 590

Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp
 595 600 605

Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met
 610 615 620

Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala
 625 630 635 640

Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys
 645 650 655

Asp Ala Gln Thr Arg Ile Thr Lys
 660

<210> 70

<211> 2004

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 70

atgaaaataa aaacagggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120
 aaaggctata acggctctcg tgaagtccgg aagaatttcg agaaagatcc cgaaattaaa 180
 gtcacccgttgc agcatccggaa taaatcgaa gagaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgttgc gtggctacgc tcaatctggc 300
 ctgttggctg aatcacccccc ggacaaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caaactgattt gcttacccggat tcgctgttgc agcgttatcg 420
 ctgatttata acaaagatctt gctgccgaac ccgcacaaaaa cctggaaaga gatcccggcg 480
 ctggataaaag aactgaaagc gaaggtaag agcgcgttgc tggttcaaccc gcaagaaccg 540
 tacttcaccc ggcgcgttat tgctgttgc gggatgaag ccataccaaa cgacgagcgt 600
 gacaccacga tgcctgcagc aatggcaaca acgttgcgc aactattaac tggcgaacta 660
 cttactcttag cttcccgca acaattaata gactggatgg aggccgataa agttgcagga 720
 ccacttctgc gtcggccct tccggctggc tggtttattt ctgataaatac tggagccgg 780
 gagcgtgggt ctcgcggat cattgcagca ctggggccag atggtaagcc ctcccgat 840
 gtagttatctt acacgcacggg gagtcaggca actatggatg aacgaaatag acagatcgct 900
 gagataggtg cctcactgtat taagcattgg gacaagagcc acccagaaac gctgggtaaa 960
 gtaaaaagatg ctgaagatca gttgggttgc ctagtgggtt acatcgaaact ggatctcaac 1020
 agcggtaaga tccttgagag ttttcggccc gaagaacgtt ttccaatgtat gaggactttt 1080
 aaagttctgc tatgtggcgc ggtattatcc cgtgttgcg ccggcaga gcaactcggt 1140
 cggccgcatac actattctca gaatgactt gttgagtact caccagtac agaaaagcat 1200
 cttacggatg gcatgacagt aagagaatta tgcaatgttgc ccataaccat gagtgataac 1260
 actgcggcca acttacttctt gacaacgatc ggaggaccga aggagctaac cgctttttt 1320
 cacaacatgg gggatcatgt aactgcgcctt gatcgatggg aaccggaaact gaatgaagcc 1380
 gacgggggtt atgcgttcaa gtatgaaaac ggcaagtacg acattaaaga cgtggcgtg 1440
 gataacgctg ggcgcgaaagc gggctgttgc tccctgggtt acctgttataa aaacaaacac 1500
 atgaatgcag acaccgatta ctccatcgca gaagctgcct ttaataaagg cgaaacagcg 1560

atgaccatca acggcccggtg ggcatggtcc aacatcgaca ccagcaaagt gaattatgg 1620
 gtaacgtac tgccgacctt caagggtcaa ccatccaaac cgttcgttgg cgtgctgagc 1680
 gcaggttata acgcccggcag tccgaacaaa gagctggcga aagagttcct cgaaaactat 1740
 ctgctgactg atgaaggctt ggaagcggtt aataaagaca aaccgctggg tgccgtacg 1800
 ctgaagtctt acgaggaaga gttggcgaaa gatccacgta ttgcccac catggaaaac 1860
 gcccagaaag gtgaaatcat gccgaacatc ccgcagatgt ccgcattctg gatgccgtg 1920
 cgtactgcgg tcatcaacgc cggcagcggt cgtcagactg tcgatgaagc cctgaaagac 1980
 ggcgcagactc gatcaccaa gtaa 2004

<210> 71

<211> 667

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 71

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr | |
| 1 | | | | | | | | 5 | | | | | | 10 | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | 20 | | | 25 | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | 35 | | | 40 | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | 50 | | | | | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| 65 | | | | | | | | 70 | | | 75 | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | | | | | 85 | | | 90 | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | 100 | | | 105 | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | Ala | Val | Arg | Tyr | Asn | Gly | Lys |
| | 115 | | | | | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu | Ala | Leu | Ser | Leu | Ile | Tyr | Asn |
| | 130 | | | | | | | 135 | | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | Thr | Trp | Glu | Glu | Ile | Pro | Ala |
| 145 | | | | | | | | 150 | | | 155 | | 160 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Lys | Glu | Leu | Lys | Ala | Lys | Gly | Lys | Ser | Ala | Leu | Met | Phe | Asn |
| | | | | | | | | 165 | | | 170 | | 175 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Glu | Pro | Tyr | Phe | Thr | Trp | Pro | Leu | Ile | Ala | Ala | Asp | Gly | Asn |
| | | | | | | | | 180 | | | 185 | | 190 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Ile | Pro | Asn | Asp | Glu | Arg | Asp | Thr | Thr | Met | Pro | Ala | Ala | Met |
| | | | | | | | | 195 | | | 200 | | 205 | | |

Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala
 210 215 220

Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly
 225 230 235 240

Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys
 245 250 255

Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly
 260 265 270

Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser
 275 280 285

Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala
 290 295 300

Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr Leu Val Lys
 305 310 315 320

Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu
 325 330 335

Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu
 340 345 350

Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val
 355 360 365

Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His
 370 375 380

Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His
 385 390 395 400

Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr
 405 410 415

Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly
 420 425 430

Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr
 435 440 445

Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Asp Gly Gly Tyr
 450 455 460

Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val
 465 470 475 480

Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu Ile
 485 490 495

Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala
 500 505 510

Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala
 515 520 525

Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu
 530 535 540

Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser
 545 550 555 560

Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe
 565 570 575

Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys
 580 585 590

Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu
 595 600 605

Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly
 610 615 620

Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val
 625 630 635 640

Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu
 645 650 655

Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
 660 665

<210> 72

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 72

atgaaaataa aaacagggtgc acgcacatccgc gcattatccg cattaaacgac gatgatgttt 60
 tccgcctcggt ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggctctcgcc tgaagtcgggta aagaaattcg agaaagatac cgaaattaaaa 180
 gtcacccgttgc agcatccggta taaactggaa gagaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aaatcaccccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttacccga tcgctgttga agcgatcc 420
 ctgatttata acaaagatct gctggcgaac ccggccaaaaa cctggaaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaacccg 540
 tacttcaccc ggcgcgtat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca taaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccctc 660
 ctgggttggacc tgattaaaaaa caaacacatg aatgcagacaca ccgattactc catcgccagaa 720
 gctgccttta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaac 780
 atcgacacca gcaaagtggaa ttatgggtga acggctactgc cgaccctcaa gggtcaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaaacg ccggcagtcgaa acacaaagag 900
 ctggcggaaag agttcctcga aaactatctg ctgactgtatg aaggctgttgc agcggtaat 960
 aaagacaaaac cgctgggtgc cgtacgcgtg aaatcgttacg aggaagagtt ggcgaaagat 1020

ccacgtattg ccgccaccat ggaaaacgcc cagaaagggtg aaatcatgcc gaacatcccg 1080
 cagatgtccg ctttctggta tgccgtgcgt actgcgggtga tcaacgccgc cagcggtcgt 1140
 cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
 agagaattat gcagtgcgtc cataaccatg agtgataaca ctgcggccaa cttacttctg 1260
 acaacgatcg gaggaccgaa ggagctaacc gctttttgc acaacatggg ggatcatgta 1320
 actcgcccttg atcggttggga accggagctg aatgaagcca taccaaacga cgagcgtgac 1380
 accacgatgc ctgcagcaat ggcaacaacg ttgcgcaaac tattaactgg cgaactactt 1440
 actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
 cttctgcgt cggcccttcc ggctggctgg tttattgtctg ataaatctgg agccggtgag 1560
 cgtgggtctc gcggtatcat tgcagcaact gggccagatg gtaagccctc cctgtatcgta 1620
 gttatctaca cgacggggag tcaggcaact atggatgaa gaaatagaca gatcgctgag 1680
 ataggtgcct cactgattaa gcattgggaa tccggcggtg gccacccaga aacgctggtg 1740
 aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg gttacatcgta actggatctc 1800
 aacagcggta agatcgttgc gagtttgc cccgaagaac gttttccaat gatgagcact 1860
 tttaaagttc tgctatgtgg cgcggattt tcccgtgtt acgcggggca agagcaactc 1920
 ggtcggcgca tacactattt tcagaatgac ttgggtgagt actcaccagt cacagaaaag 1980
 catttacgg atggcaagtg a 2001

<210> 73

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 73

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Leu | Ala | Leu | Ser | Ala | Leu | Thr |
| 1 | | | | | | | | | 5 | | | | | 10 | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Leu | Ala | Lys | Ile | Glu | Glu | Gly | Lys |
| | | | | | | | | 20 | | 25 | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Leu | Ala | Glu |
| | | | | | | | | 35 | | 40 | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | | | | | | | | 50 | | 55 | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| | | | | | | | | 65 | | 70 | | 75 | | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Gly | Tyr |
| | | | | | | | | 85 | | 90 | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | 100 | | 105 | | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Leu | Tyr | Pro | Phe | Thr | Trp | Asp | Ala | Val | Arg | Tyr | Asn | Gly | Lys |
| | | | | | | | | 115 | | 120 | | | 125 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Ala | Tyr | Pro | Ile | Ala | Val | Glu | Ala | Leu | Ser | Leu | Ile | Tyr | Asn |
| | | | | | | | | 130 | | 135 | | | 140 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Leu | Leu | Pro | Asn | Pro | Pro | Lys | Thr | Trp | Glu | Glu | Ile | Pro | Ala |
| | | | | | | | | 145 | | 150 | | | 155 | | 160 |

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys Gly Met Thr Val
 385 390 395 400
 Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala
 405 410 415
 Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 420 425 430
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 435 440 445
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 450 455 460

Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 465 470 475 480

Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 485 490 495

Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 500 505 510

Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 515 520 525

Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 530 535 540

Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 545 550 555 560

Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly His Pro
 565 570 575

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 580 585 590

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 595 600 605

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 610 615 620

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 625 630 635 640

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 645 650 655

Val Thr Glu Lys His Leu Thr Asp Gly Lys
 660 665

<210> 74

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 74

 atgaaaataa aaacaggtgc acgcacccctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acgggtctcgc tgaagtccgt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccgttg agcatccgaa taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccggc tcgctgtga agcgatcg 420
 ctgattata acaaagatct gctgccgaac ccggaaaaaa cctggaaaga gatcccggcg 480

ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
 ctggtgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
 gctgcctta ataaaggcga aacagcgatg accatcaacg gcccgtggc atggtccaac 780
 atcgacacca gcaaagtgaa ttatggtgta acggtaactgc cgaccctcaa gggtcaacca 840
 tccaaaccgt tcgttggcgt gctgagcgcgca gttatcactg ccgcccagtcc gaacaaagag 900
 ctggcggaaag agttccctcgaa aactatctg ctgactgtatg aaggctcgga agcggttaat 960
 aaagacaaac cgctgggtgc cgtagcgcgtg aagtcttaacg aggaagagtt ggcgaaagat 1020
 ccacgtattg cgcaccat ggaaaacgcc cagaaagggtg aaatcatgccc gaacatcccg 1080
 cagatgtccg ctttctggta tgccgtgcgt actgcgggtga tcaacgcgcg cagcggtcgt 1140
 cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
 agagaattat gcagtgcgtc cataaccatg agtgataaaca ctgcggccaa cttacttctg 1260
 acaacgatcg gaggaccgaa ggagctaaccgcgttgc acaacatggg gatcatgtta 1320
 actcgccttg atcggtggaa accggagctg aatgaagcaca tccaaacgca cgagcgtgac 1380
 accacatgcg ctgcagcaat ggcaacaacg ttgcgcacaaacttataactgg cgaactactt 1440
 actctagct cccggcaaca attaatagac tggatggagg cggataaaagt tgcaggacca 1500
 cttctgcgt cggcccttcc ggctggctgg ttattgcgt ataaatctgg agccggtgag 1560
 cgtgggtctc gcggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
 gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgctgag 1680
 ataggtgcct cactgattaa gcattggga tccggcggtg gccacccaga aacgctggtg 1740
 aaagtaaaag atgctgaaga tcagttgggt gcacgagtttgcgttacatcgaaactggatctc 1800
 aacagcggta agatccttga gagtttcgc cccgaagaac gtttccaat gatgagact 1860
 tttaaagttc tgctatgtgg cgcggtattatcccggttgc acgcccggca agagcaactc 1920
 ggtcggccgca tacactattc tcagaatgac ttgggttgagt actcaccagt cacagaaaaag 1980
 catcttacgg aagtgaagag cactagttag 2010

<210> 75

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 75

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Ala | Arg | Ile | Lys | Ala | Lys | Ser | Ala | Lys | Thr |
| 1 | | | | | | | | 5 | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Thr | Met | Met | Phe | Ser | Ala | Ser | Ala | Lys | Ile | Glu | Glu | Gly | Lys | | |
| | | | | | | | | 20 | | 25 | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Leu | Val | Ile | Trp | Ile | Asn | Gly | Asp | Lys | Gly | Tyr | Asn | Gly | Lys | | |
| | | | | | | | | 35 | | 40 | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Lys | Phe | Glu | Lys | Asp | Thr | Gly | Ile | Lys | Val | Thr | Val | Glu |
| | | | | | | | | 50 | | 55 | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asp | Lys | Leu | Glu | Glu | Lys | Phe | Pro | Gln | Val | Ala | Ala | Thr | Gly |
| | | | | | | | | 65 | | 70 | | | 75 | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Gly | Pro | Asp | Ile | Ile | Phe | Trp | Ala | His | Asp | Arg | Phe | Gly | Tyr | |
| | | | | | | | | 85 | | 90 | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ser | Gly | Leu | Leu | Ala | Glu | Ile | Thr | Pro | Asp | Lys | Ala | Phe | Gln |
| | | | | | | | | 100 | | 105 | | | 110 | | |

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350

Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365

Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380

Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys Gly Met Thr Val
 385 390 395 400

Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala
 405 410 415

Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 420 425 430
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 435 440 445
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 450 455 460
 Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 465 470 475 480
 Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 485 490 495
 Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 500 505 510
 Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 515 520 525
 Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 530 535 540
 Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 545 550 555 560
 Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly His Pro
 565 570 575
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 580 585 590
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 595 600 605
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 610 615 620
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 625 630 635 640
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 645 650 655
 Val Thr Glu Lys His Leu Thr Glu Val Lys Ser Thr Ser
 660 665

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 76
 ggaccaggat ccatgaaaat aaaaacaggt 30

<210> 77
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 77
 Gly Gly Ser Gly His His His His His His His His
 1 5 10

<210> 78
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 78
 gctttctca cccagaaaacg ctgggt 26

<210> 79
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 79
 ctgattaagc attgggacaa gagccactga agaga 35

<210> 80
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 80
 caccaggaaa cgctgggt 18

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<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 81
ctgattaagc attgggacaa gagc 24

<210> 82
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 82
gtggctcttg tcccaatgct taatcag 27

<210> 83
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 83
caccagcggtt tctgg 15

<210> 84
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 84
ctgattaagc attgggacaa gagccaccca gaaacgctgg tg 42

<210> 85
<211> 33
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 85
ggatccggcg gtggccaccc agaaaacgctg gtg

33

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 86
ctgat~~ta~~aggc attggggatc c

21

<210> 87
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 87
gatccggcg~~g~~ tggccaccc~~a~~ gaaaacgctgg tg

32

<210> 88
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 88
ctgat~~ta~~aggc attggg

16

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 89
gatccccaa~~t~~ gcttaatcag

20

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<210> 90
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
      }

<400> 90
caccagcggt tctgggtggc caccgccc                                28

<210> 91
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 91
ctgatataaagc attggggatc cggcggtggc cacccagaaa cgctggtg                                48

<210> 92
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 92
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<210> 93
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 93
ctgattgctg ctgac                                15

<210> 94
<211> 18
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 94
gacgggggtt atgcgttc

18

<210> 95
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 95
gaacgcataa ccccc

15

<210> 96
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 96
cccgtagca gcaatcag

18

<210> 97
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 97
ctgattgctg ctgacggg

18

<210> 98
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 98
ctgatcgcta ggagacggcg a

<210> 99
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 99
His His His His His His
1 5